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L2: Entry 1 of 22 File: USPT May 21, 2002

DOCUMENT-IDENTIFIER: US 6391580 B1
TITLE: Ras proteins

Brief Summary Paragraph Right (5):
The Ras subfamily already indicated supra are essential in transducing signals from receptor tyrosine kinases (RTKs) to a series of serine/threonine kinases which control cell growth and differentiation. Activated Ras genes were initially found in human cancers and subsequent studies confirmed that Ras function is critical in the determination of whether cells continue to grow or become terminally differentiated. Stimulation of cell surface receptors activates Ras which, in turn, activates cytoplasmic kinases. The kinases translocate to the nucleus and activate key transcription factors that control gene expression and protein synthesis. (Barbacid, M. (1987)Ann. Rev Biochem. 56:779-827, Treisman, R. (1994) Curr. Opin. Genet. Dev. 4:96-98.) Mutant Ras proteins, which bind but can not hydrolyze GTP, are permanently activated, and cause continuous cell proliferation or cancer. TC2 1, a Ras-like protein, is found to be highly expressed in a human teratocarcinoma cell line. (Drivas, G. T. et al. (1990) Mol. Cell. Biol. 10: 1793-1798.) Rin and Rit are characterized as membrane-blinding, Ras-like proteins without the lipid-binding CAAX motif and carboxy terminal cysteine. (Lee, C.-H. J. et al. (1996) J. Neurosci. 16: 6784-6794.) Further, Rin is shown to localize in neurons and have calcium-dependant calmodulin-binding activity.

Brief Summary Paragraph Right (111):
In one embodiment, an antagonist of RASP may be administered to a subject to treat or prevent a cancer associated with increased expression or activity of RASP. Such a cancer may include, but is not limited to, adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. In one aspect, an antibody which specifically binds RASP may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express RASP.

Brief Summary Paragraph Right (157):
Polynucleotide sequences encoding RASP may be used for the diagnosis of a disorder associated with expression of RASP. Examples of such a disorder include, but are not limited to, cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and immune disorders such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis,

ulcerative colitis, Werner syndrome, and complications of cancer, hemodialysis, and extracorporeal circulation; viral, bacterial, fungal, parasitic, protozoal, and helminthic infections; and trauma. The polynucleotide sequences encoding RASP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and ELISA assays; and in microarrays utilizing fluids or tissues from patients to detect altered RASP expression. Such qualitative or quantitative methods are well known in the art.

Other Reference Publication (6):
Drivas, G.T. et al., "Characterization of Four Novel ras-Like Genes Expressed in a Human Teratocarinoma Cell Line", Mol. Cell. Biol. 10: 1793-1798 (1990).

☐ **1:** BF332597. PM0-BT0730-280300...[gi:11303345] PubMed, Taxonomy

IDENTIFIERS

dbEST Id:	**6808290**
EST name:	PM0-BT0730-280300-001-d02
GenBank Acc:	BF332597
GenBank gi:	11303345

CLONE INFO

DNA type:	cDNA

PRIMERS

Sequencing:	puc 18 forward
PolyA Tail:	Unknown

SEQUENCE

ATCCGGGGAGCGACAGTCAGTATTCACATCGCTGGTCTGAGCAAGCTTGCAAGGAACTTG
ACCAAATATATTAAGTTAACAAAATTTTGTGGTGGCAACTTCTGACATGTTCTCCACAAG
TCTTGAAGTTTTTGTCTTGATCCTGCACACTTGCAACTTGTGTCCATTCTTCATACAGAT
TAAAAGTCATCAAAGGTTCAGGCAATTCCCGTAAATAGGATTTTAAAGCACCTGCTACAG
TATGGGGGTCTGAATAGAACTCATCCAGGTGAGAAGTAGAACAGTCCAAAGCAGCTTTCA
GCTTCTTTAACTTGGAGGCCCCAGCCCCAATTCGGAAAAGGCCCTCCTCCTTCATGCCTG
TCTCCAGAAGCAGCATGACACAGGCTTCAATGGGCAGCGCAATCTCGCGCCCGCTCCTCT
TCAGGTGTTCTTCTAGGGGAGTCCCAAAGGCTGGTTTTTCCGCCCACTTATCTTGATGGG
CTCGCATTTCGGGGAGGGTCTTTTCTAAGACTGCTAATGCTTTTCTATGGTAATCTGCTT
GGGCTTCTAATAACGTAACAAAGAATTTGCCATACTCCCCGGGATA

Quality:	High quality sequence stops at base: 11
Entry Created:	Nov 22 2000
Last Updated:	Nov 22 2000

COMMENTS

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0-BT0730-280)

LIBRARY

Lib Name:	BT0730
Organism:	Homo sapiens
Organ:	breast
Develop. stage:	Adult
Vector:	puc18
R. Site 1:	SmaI
R. Site 2:	SmaI
Description:	A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

SUBMITTER

Name:	Simpson A.J.G.
Lab:	Laboratory of Cancer Genetics
Institution:	Ludwig Institute for Cancer Research
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Tel:	+55-11-2704922
Fax:	+55-11-2707001
E-mail:	asimpson@ludwig.org.br

CITATIONS

Medline UID:	20202663
Title:	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Authors:	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., Simpson,A.J.
Citation:	Proc. Natl. Acad. Sci. U.S.A. 97 (7): 3491-6 2000

MAP DATA

Revised: October 24, 2001.

L3 ANSWER 10 OF 21 MEDLINE DUPLICATE 8

ACCESSION NUMBER: 2001236084 MEDLINE
DOCUMENT NUMBER: 21153423 PubMed ID: 11255007
TITLE: ERGL, a novel gene related to ERGIC-53 that is highly expressed in normal and neoplastic prostate and several other tissues.
AUTHOR: Yerushalmi N; Keppler-Hafkemeyer A; Vasmatzis G; Liu X F; Olsson P; Bera T K; Duray P; Lee B; Pastan I
CORPORATE SOURCE: Laboratory of Molecular Biology, National Cancer Institute,
National Institutes of Health, 37/4E16, 37 Convent Drive MSC 4255, 20892-4255, Bethesda, MD, USA.
SOURCE: GENE, (2001 Mar 7) 265 (1-2) 55-60.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010503

AB We have identified a new gene, that is highly expressed in normal and neoplastic prostate, and is also expressed in cardiac atrium, salivary gland, spleen and selective cells in the CNS. Database analyses of ESTs indicated prostate specificity but experimental results showed the expression in other tissues. The full length transcript is 1800 bp with an open reading frame of 526 aa. The amino-terminal 230 residues of the expressed protein has high homology to a family of **lectins**, especially to the sugar binding domain of ERGIC-53. We therefore designate the new gene ERGL (ERGIC-53-like). There is a transmembrane domain at amino acid positions 468-482 suggesting that the product of ERGL is a type-I membrane protein. In prostate there are two fully processed transcripts one of which is a **splice variant** with a deletion in the region of the transmembrane domain of the protein.

L40 ANSWER 3 OF 4 MEDLINE
ACCESSION NUMBER: 2001522883 MEDLINE
DOCUMENT NUMBER: 21454106 PubMed ID: 11570368
TITLE: "**In silico** experiments"--yes, but the great western cowboy "random chance" is still alive.
COMMENT: Comment on: Fertil Steril. 1994 Feb;61(2):248-51
Comment on: Fertil Steril. 2000 Dec;74(6):1108-13
Comment on: Fertil Steril. 2000 Mar;73(3):536-40
Comment in: Fertil Steril. 2001 Sep;76(3):639-40
AUTHOR: Stricker R B; Steinleitner A
SOURCE: FERTILITY AND STERILITY, (2001 Sep) 76 (3) 637-9.
Journal code: 0372772. ISSN: 0015-0282.
PUB. COUNTRY: United States
Commentary
Letter
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010926
Last Updated on STN: 20020419
Entered Medline: 20011011

L40 ANSWER 2 OF 4 MEDLINE

ACCESSION NUMBER:	2001522882 MEDLINE
DOCUMENT NUMBER:	21454105 PubMed ID: 11570367
TITLE:	"**In silico** experiments"--yes, but the great western cowboy "random chance" is still alive.
COMMENT:	Comment on: Fertil Steril. 2000 Dec;74(6):1108-13 Comment in: Fertil Steril. 2001 Sep;76(3):639-40
AUTHOR:	Sher G; Fisch J D
SOURCE:	FERTILITY AND STERILITY, (2001 Sep) 76 (3) 636-7; discussion 638-9. Journal code: 0372772. ISSN: 0015-0282.
PUB. COUNTRY:	United States
	Commentary
	Letter
LANGUAGE:	English
FILE SEGMENT:	Priority Journals
ENTRY MONTH:	200110
ENTRY DATE:	Entered STN: 20010926 Last Updated on STN: 20020419 Entered Medline: 20011011

L3 ANSWER 19 OF 55 MEDLINE

ACCESSION NUMBER: 2001418683 MEDLINE
DOCUMENT NUMBER: 21360614 PubMed ID: 11466977
TITLE: Mining of assembled expressed sequence tag (EST) data for protein families: application to the G protein-coupled receptor superfamily.
AUTHOR: Conklin D; Yee D P; Millar R; Engelbrecht J; Vissing H
CORPORATE SOURCE: MRC Reproductive Biology Unit, Edinburgh.
SOURCE: Brief Bioinform, (2000 Feb) 1 (1) 93-9.
Journal code: 100912837. ISSN: 1467-5463.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

AB The availability of large expressed **sequence tag** (**EST**) databases has led to a revolution in the way new genes are identified. Mining of these databases using known protein sequences as queries is a powerful technique for discovering orthologous and paralogous genes. The scientist is often confronted, however, by an enormous amount of search output owing to the inherent redundancy of **EST** data. In addition, high search sensitivity often **cannot** be achieved using only a single member of a protein superfamily as a query. In this paper a technique for addressing both of these issues is described. Assembled **EST** databases are queried with every member of a protein superfamily, the results are integrated and false positives are pruned from the set. The result is a set of assemblies enriched in members of the protein superfamily under consideration. The technique is applied to the G protein-coupled receptor (GPCR) superfamily in the construction of a GPCR Resource. A novel full-length human GPCR identified from the GPCR Resource is presented, illustrating the utility of the method.

L26 ANSWER 8 OF 35 MEDLINE DUPLICATE 7

ACCESSION NUMBER: 2001389170 MEDLINE
DOCUMENT NUMBER: 21336737 PubMed ID: 11443211
TITLE: Expression of reduced nicotinamide adenine dinucleotide phosphate oxidase (ThoX, LNOX, Duox) genes and proteins in human thyroid tissues.
AUTHOR: Caillou B; Dupuy C; Lacroix L; Nocera M; Talbot M; Ohayon R; Deme D; Bidart J M; Schlumberger M; Virion A
CORPORATE SOURCE: Department of Pathology, Institut Gustave-Roussy, 94805 Villejuif, France.
SOURCE: JOURNAL OF CLINICAL ENDOCRINOLOGY AND METABOLISM, (2001 Jul) 86 (7) 3351-8.
Journal code: 0375362. ISSN: 0021-972X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802

AB The large homolog of NADPH oxidase flavoprotein LNOX2, and probably LNOX1, are flavoproteins involved in the thyroid H(2)O(2) generator. Western blot analysis of membrane proteins from normal human thyroid, using antipeptide antibodies, indicated that LNOX1,2 are 164-kDa glycoproteins and that N-glycosylated motifs account for at least 10-20 kDa of their total apparent molecular mass. Northern blot analysis of 23 different human tissues demonstrated that LNOX2 messenger RNA (**mRNA**) is strongly **expressed** only in the thyroid gland, although blast analysis of **expressed** sequence **tags databases** indicated that LNOX genes are also expressed in some nonthyroid cells. We investigated LNOX1,2 gene and **protein expressions** in normal and pathological human thyroid tissues using real-time kinetic quantitative PCR and antipeptide antibodies, respectively. In normal tissue, LNOX1,2 are localized at the apical pole of thyrocytes. Immunostaining for LNOX1,2 was heterogeneous, inside a given follicle, with 40-60% of positive follicular cells. Among normal and pathological tissues, variations of LNOX1 and LNOX2 mRNA levels were parallel, suggesting a similar regulation of both gene **expressions**. Whereas LNOX **mRNAs** seemed slightly affected in benign disease, the **expression** of **protein** was highly variable. In multinodular goiters, 40-60% of cells were stained. In hypofunctioning adenomas, LNOX immunostaining was highly variable among follicles, whereas sodium/iodide (Na+/I-) symporter immunostaining was decreased. In hyperfunctioning thyroid tissues, only few cells (0-10%) were weakly stained, whereas sodium/iodide symporter staining was found in the majority of follicular cells. In conclusion, LNOX proteins are new apical glycoproteins with a regulation of expression that differs from other thyroid markers.

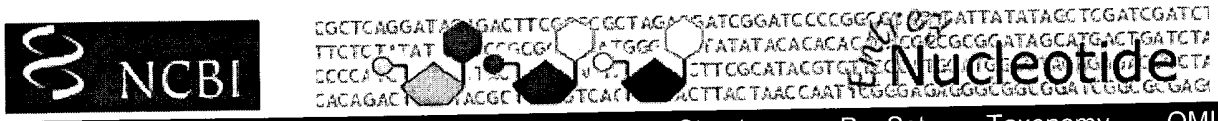
L20 ANSWER 10 OF 13 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:519168 BIOSIS
DOCUMENT NUMBER: PREV200100519168
TITLE: DNA chips designed to detect alternative splicing using LEADS.
AUTHOR(S): Wasserman, Alon (1); Shoshan, Avi (1); Grebinskiy, Vladimir (1)
CORPORATE SOURCE: (1) Compugen Inc., Jamesburg, NJ USA
SOURCE: International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 63. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference Miami Beach, Florida, USA September 12-15, 2000
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We design chips enabling the detection of alternative **splice** variants. The design optimally chooses segments representing the **splice** variants of each gene. Probes are selected from each segment using criteria including specificity, distance from the 3' end, sequence quality, GC content, and so on. The designs are based on the LEADS software that clusters and assembles **ESTs**, known mRNAs and genomic data. For each gene, it produces a list of predicted mRNA transcripts, each a different **splice** variant. Multiply covered areas are used to detect and eliminate sequencing errors. These areas are also used for the detection of polymorphisms, which can be used in genotyping chips. Having good designs is crucial to extract meaningful information from chip experiments. Designs not using all available data, **splice** variants and sequencing errors might lead to useless probes and misleading results. It is believed that at least 35% of human genes have alternative **splice** variants, and it is important to distinguish between their **expression patterns**. This is achieved by choosing probes that are unique to some of the variants. If one just wishes to measure the overall expression level of the gene, probes that are common to all the variants can be chosen.

L20 ANSWER 11 OF 13 MEDLINE DUPLICATE 8

ACCESSION NUMBER: 2000082975 MEDLINE
DOCUMENT NUMBER: 20082975 PubMed ID: 10613851
TITLE: Frequent alternative splicing of human genes.
AUTHOR: Mironov A A; Fickett J W; Gelfand M S
CORPORATE SOURCE: State Center of Biotechnology NIIGenetika, Moscow, 113545, Russia.
SOURCE: GENOME RESEARCH, (1999 Dec) 9 (12) 1288-93.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000204
Last Updated on STN: 20000204
Entered Medline: 20000127

AB Alternative **splicing** can produce variant proteins and **expression patterns** as different as the products of different genes, yet the prevalence of alternative **splicing** has not been quantified. Here the **spliced** alignment algorithm was used to make a first inventory of exon-intron structures of known human genes using **EST** contigs from the TIGR Human Gene Index. The results on any one gene may be incomplete and will require verification, yet the overall trends are significant. Evidence of alternative **splicing** was shown in 35% of genes and the majority of **splicing** events occurred in 5' untranslated regions, suggesting wide occurrence of alternative regulation. Most of the alternative **splices** of coding regions generated additional protein domains rather than alternating domains.



1: AU123421. AU123421 NT2RM2 H...[gi:10948137]

MapView, Taxonomy, LinkOut

IDENTIFIERS

dbEST Id: 6548333
EST name: AU123421
GenBank Acc: AU123421
GenBank gi: 10948137

CLONE INFO
Clone Id: NT2RM2000260 (5')
DNA type: cDNA

PRIMERS
PolyA Tail: Unknown

SEQUENCE

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CCAGCTCTCAGCACCCCGGAGGTACTCCAGCAGCTTGTCTCCAATCCAAGCTCCCAATCA
CCCACCGCCGCAGCCCCCTACGCAGGCCACGCCACTGATGCACACCAAACCCAATAGCCA
GGGCCCTCCCAACCCCATGGCATTGCCCAGTGAGCATGGACTTGAGCAGCCATCTCACAC
CCCTCCCCAGACTCCAACGCCCCCCAGTACTCCGCCCCTAGGAAAACAGAACCCCAGTCT
GCCAGCTCCTCAGACCCTGGCAGGGGGTAACCCTGAAACTGCACAGCCACATGCTGGAAC
CTTACCGAGACCGAGACCAGTACCAAAGCCAAGGAACCGGCCCAGCGTGCCCCCACCCCC
CCAACCTCCTGGTGTCCACTCAGCTGGGGACAGCAAGCCTCACCAACACAGCACCAACAG
CTTCCAAGATAGTAACAGGGTTTCAGAACCGCATCGCAGCATCTTTCCTGAAATGCACTC
AGACTCAGCCAGCAAAGACGTTGCCTGGGCCGCATCCTGCTGGATATAGACAATTGATAC
CGGAGAAGCACTGCCCCTGTTGAAGGAAAAGGCCCTTTTCCANGCCCTTCCAACAANTTT
CCAACCCTGGN

Entry Created: Oct 23 2000
Last Updated: Oct 23 2000

COMMENTS

HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Helix Research Institute; cDNA library construction:
Department of Virology, Institute of Medical Science,
University of Tokyo, and Helix Research Institute.

LIBRARY
Lib Name: NT2RM2
Organism: Homo sapiens
Cell type: teratocarcinoma
Cell line: NT2
Vector: pME18SFL3
Description: mRNA from uninduced NT2 neuronal precursor cells

SUBMITTER
Name: Takao Isogai
Lab: Genomics Laboratory

Institution: Helix Research Institute
Address: 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
E-mail: genomics@hri.co.jp

CITATIONS

Title: HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)

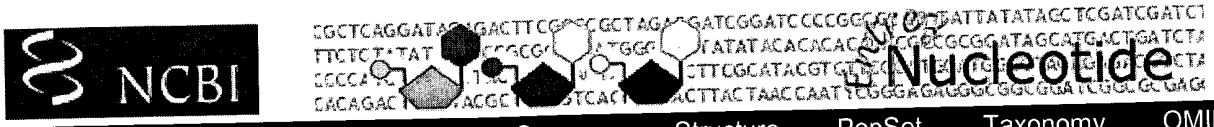
Authors: Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto ,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano ,S., Isogai,T.

Year: 2000

Status: Unpublished

MAP DATA

Revised: October 24, 2001.



1: AU142211. AU142211 VESEN1 H...[gi:11003732]

MapView, Taxonomy, LinkOut

IDENTIFIERS

dbEST Id:	**6571226**
EST name:	AU142211
GenBank Acc:	AU142211
GenBank gi:	11003732

CLONE INFO

Clone Id:	VESEN1000364 (5')
DNA type:	cDNA

PRIMERS

PolyA Tail:	Unknown

SEQUENCE

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ACCAAGCTCACAAATCCTNAGGAACCAACTTTCAGGGGCTTCCATCAAAAATAGATACTC
TAAAGGAAGAGATGGATGAAGCTGGAAATAAAGTAGAACAGTGCAAGGATCAACTTGCAG
CAGACATGTACAACTTTATGGCCAAAGAAGGGGAGTATGGCAAATTCTTTGTTACGTTAT
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AAATGCGAGCCCATCAAGATAAGTGGGCGGAAAAACCAGCCTTTGGGACTCCCCTAGAAG
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ACCCCCATGCTGTAGCAGGTGCTTTAAAATCCTATTTACGGGAATTGCCTGAACCTTTGA
TGACTTTTAATCTGTATGAAGAATGGACACAAGTTGCAAGTGTGCAGGATCAAGACAAAA
AACTTCAAGACTTGTGGAGAACATGTCAGAAGTTGCCACCACAAAATTTTGGTAACTTTA
GATATTTGATCAAGTTNCNTTGCAAAGCTTGCTCAGACCAGCCGATGTGAATAAAATGAC
TCCCNGAACATTGC

Entry Created:	Oct 25 2000
Last Updated:	Oct 25 2000

COMMENTS

HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Helix Research Institute; cDNA library construction:
Department of Virology, Institute of Medical Science,
University of Tokyo, and Helix Research Institute.

LIBRARY

Lib Name:	VESEN1
Organism:	Homo sapiens
Cell type:	umbilical vein endothelial cell (HUVEC)
Vector:	pME18SFL3
Description:	primary endothelial cells

SUBMITTER

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Lab:	Genomics Laboratory
Institution:	Helix Research Institute

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Tel: 81-438-52-3951
Fax: 81-438-52-3952
E-mail: genomics@hri.co.jp

CITATIONS

Title: HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii ,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., Isogai,T.)

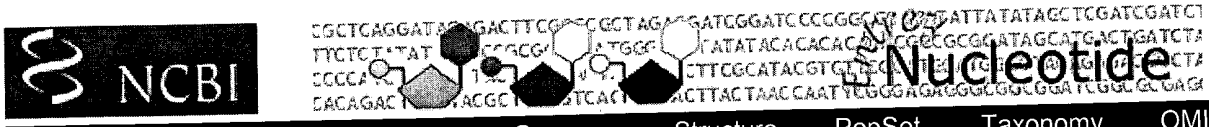
Authors: Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama ,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., Isogai ,T.

Year: 2000

Status: Unpublished

MAP DATA

Revised: October 24, 2001.



1: AU133334. AU133334 NT2RP4 H...[gi:10993873]

MapView, Taxonomy, LinkOut

IDENTIFIERS

dbEST Id: **6562293**
EST name: AU133334
GenBank Acc: AU133334
GenBank gi: 10993873

CLONE INFO
Clone Id: NT2RP4001849 (5')
DNA type: cDNA

PRIMERS
PolyA Tail: Unknown

SEQUENCE

ATGCAAGAAGCATCGACTCAGCTGGAAGACTCTCTCCTGGGGAAGATGCTGGAGACGTGT
GGAGATGCTGAGAATCAGCTGGCTCTCGAGCTCTCCCAGCACGAAGTCTTTGTTGAGAAG
GAGATCGTGGACCCTCTGTACGGCATAGCTGAGGTGGAGATTCCCAACATCCAGAAGCAG
AGGAAGCAGCTTGCAAGATTGGTGTTAGACTGGGATTCAGTCAGAGCCAGGTGGAACCAA
GCTCACAAATCCTCAGGAACCAACTTTCAGGGGCTTCCATCAAAAATAGATACTCTAAAG
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ATGTACAACTTTATGGCCAAAGAAGGGGAGTATGGCAAATTCTTTGTTACGTTATTAGAA
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CGAGCCCATCAAGATAAGTGGGCGGAAAAACCAGCCTTTGGGACTCCCCTAGCAGAACAC
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AAGCTGAAAGCTGCTTTGGACTGGTCTACTTCTCACCTGGATGAGTTCTATTCAGACCCC
CATGCTGTAGCAGGTGCTTTAAAATCCTATTTACCGGAATTGNCTGACCTTTGATGACTT
TTAATCTGGATGAANAATGGNCCCAG

Entry Created: Oct 24 2000
Last Updated: Oct 24 2000

COMMENTS

HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Helix Research Institute; cDNA library construction:
Department of Virology, Institute of Medical Science,
University of Tokyo, and Helix Research Institute.

LIBRARY
Lib Name: NT2RP4
Organism: Homo sapiens
Cell type: teratocarcinoma
Cell line: NT2
Vector: pME18SFL3
Description: mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction

SUBMITTER
Name: Takao Isogai

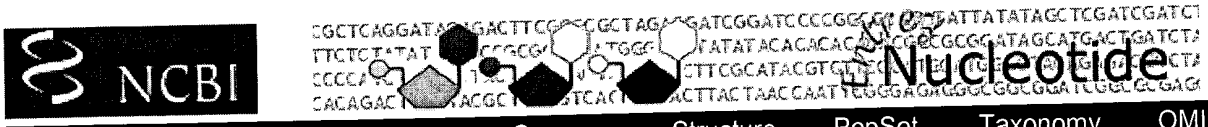
Lab: Genomics Laboratory
Institution: Helix Research Institute
Address: 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
E-mail: genomics@hri.co.jp

CITATIONS

Title: HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y., Isogai,T.)
Authors: Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto ,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho ,Y., Isogai,T.
Year: 2000
Status: Unpublished

MAP DATA

Revised: October 24, 2001.



☐ 1: BE883450. 601511009F1 NIH_M...[gi:10332226] MapView, Taxonomy, Traces, LinkOut

IDENTIFIERS

dbEST Id:	**6167123**
EST name:	601511009F1
GenBank Acc:	BE883450
GenBank gi:	10332226

CLONE INFO

Clone Id:	IMAGE:3912458 (5')
Plate:	LLAM9731 Row: a Column: 03
DNA type:	cDNA

PRIMERS

PolyA Tail:	Unknown

SEQUENCE

CGATTGTGTTAGGCCCTAACTTGTTATGGGCCAGAAATGAAGGAACACTTGCTGAAATGG
CAGCAGCCACATCCGTCCATGTGGTTGCAGTGATTGAACCCATCATTCAGCATGCCGACT
GGTTCTTCCCTGAAGAGGTGGAATTTAATGTATCAGAAGCATTTGTACCTCTCACCACCC
CGAGTTCTAATCACTCATTCCACACTGGAAACGACTCTGACTCGGGGACCCTGGAGAGGA
AGCGGCCTGCTAGCATGGCGGTGATGGAAGGAGACTTGGTGAAGAAGGAAAGTCCTCCCA
AACCGAAGGACCCTGTATCTGCAGCTGTGCCAGCACCAGGAGAAACAACAGTCAGATAGC
ATCTGGCCAAAATCAGCCCCAGGCAGCTGCTGGCTCCCACCAGCTCTCCATGGGCCAACC
TCACAATGCTGCAGGGCCCAGCCCGCATACACTGCGCCGAGCTGTTAAAAACCC

Quality:	High quality sequence stops at base: 474
Entry Created:	Sep 26 2000
Last Updated:	Oct 20 2000

COMMENTS

Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

LIBRARY

Lib Name:	NIH_MGC_71
Organism:	Homo sapiens
Organ:	uterus
Tissue type:	leiomyosarcoma
Lab host:	DH10B (phage-resistant)
Vector:	pCMV-SPORT6
R. Site 1:	NotI
R. Site 2:	SalI
Description:	Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb.

SUBMITTER

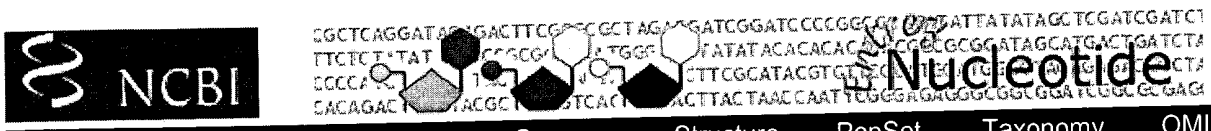
Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Institutes of Health, Mammalian Gene Collection (MGC)
Authors: NIH-MGC http://mgc.nci.nih.gov/
Year: 1999
Status: Unpublished

MAP DATA

Revised: October 24, 2001.



☐ 1: BF569925. 602185873F1 NIH_M...[gi:11643637] MapView, Taxonomy, Traces, LinkOut

IDENTIFIERS

dbEST Id:	**7051766**
EST name:	602185873F1
GenBank Acc:	BF569925
GenBank gi:	11643637

CLONE INFO

Clone Id:	IMAGE:4309938 (5')
Plate:	LLCM1184 Row: b Column: 19
DNA type:	cDNA

PRIMERS

PolyA Tail:	Unknown

SEQUENCE

GGCCCGCTGGCCCAGAGCCCCCTCCCCAGAGCTCTAGGGCTGAAAGCAGCTCTGGGGGTG
GGACTGTCCCCTCTTCCGCGGGCATACTGGAGCAGGGGCCGAGCCCAGGCGACGGCAGTC
CTCCCAAACCGAAGGACCCTGTATCTGCAGCTGTGCCAGCACCAGGGAGAAACAACAGTC
AGATAGCATCTGGCCAAAATCAGCCCCAGGCAGCTGCTGGCTCCCACCAGCTCTCCATGG
GCCAACCTCACAATGCTGCAGGGCCCAGCCCGCATACACTGCGCCGAGCTGTTAAAAAAC
CCGCTCCAGCACCCCCGAAACCGGGCAACCCACCTCCTGGCCACCCCGGGGGCCAGAGTT
CTTCAGGAACATCTCAGCATCCACCCAGTCTGTCACCAAAGCCACCCACCCGAAGCCCCT
CTCCTCCCACCCAGCACACGGGCCAGCCTCCAGGCAGCCCTCCGCCCCCTCCCAGCTCTC
AGCACCCCGGAGGTACTCCAGCAGCTTGTCTCCAATCCAAGCTCCCAATCACCCACCGCC
GCAGCCCCCTACGCAGGCCACGCCACTGATGCACACCAAAG

Quality:	High quality sequence stops at base: 579
Entry Created:	Dec 11 2000
Last Updated:	Dec 12 2000

COMMENTS

Tissue Procurement: Linehan
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

LIBRARY

Lib Name:	NIH_MGC_45
Organism:	Homo sapiens
Organ:	kidney
Tissue type:	renal carcinoma (ascites)
Lab host:	DH10B (phage-resistant)
Vector:	pOTB7
R. Site 1:	XhoI
R. Site 2:	EcoRI
Description:	cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G

). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |

SUBMITTER

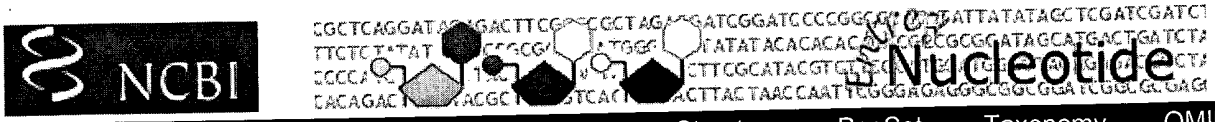
Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Institutes of Health, Mammalian Gene Collection (MGC)
Authors: NIH-MGC http://mgc.nci.nih.gov/
Year: 1999
Status: Unpublished

MAP DATA

Revised: October 24, 2001.



☐ 1: BE890141. 601513120F1 NIH_M...[gi:10348166] MapView, Taxonomy, Traces, LinkOut

IDENTIFIERS

dbEST Id:	**6173835**
EST name:	601513120F1
GenBank Acc:	BE890141
GenBank gi:	10348166

CLONE INFO

Clone Id:	IMAGE:3914525 (5')
Plate:	LLAM9736 Row: g Column: 06
DNA type:	cDNA

PRIMERS

PolyA Tail:	Unknown

SEQUENCE

CTCAGCACCCCGGAGGTACTCCAGCAGCTTGTCTCCAATCCAAGCTCCCAATCACCCACC
GCCGCAGCCCCCTACGCAGGCCACGCCACTGATGCACACCAAACCCAATAGCCAGGCCCT
CCCAACCCCATGGCATTGCCCAGTGAGCATGGACTTGAGCAGCCATCTCACACCCCTCCC
CAGACTCCAACGCCCCCCAGTACTCCGCCCCTAGGAAAACAGAACCCCAGTCTGCCAGCT
CCTCAGACCCTGGCAGGGGGTAACCCTGAAACTGCACAGCCACATGCTGGAACCTTACCG
AGACCGAGACCAGTACCAAAGCCAAGGAACCGGCCCAGCGTGCCCCCACCCCCCCAACCT
CCTGGTGTCCACTCAGCTGGGGACAGCAGCCTCACCAACACAGCACCAACAGCTTCCAAG
ATAGTAACAGACTCCAATTCCAGGCTTTCAGAACCGCATCCGCAGCATCTTTCCTGAAAT
GCACTCAGACTCAGCCAGCAAAGACGTGCCTGGCCGCATCCTGCTGGATATAGACAATGA
TACCGAGAGCACTGCCCTGTGAAAGAAAGCCCTTTCCCAGCCTTCCACACTTCCACCCTG
GAGAGTGGAACCAGGGGCAGGCGAACTCTTTCTTTTGCGGACCGAACAGTGAAAAGCTTC
ACCTGGAGGACACCCCCGAGGCCCACTGTGCGGGCACTGGGCTTTGGCGCGCCCAGGGAA
ACTGGC

Quality:	High quality sequence stops at base: 590
Entry Created:	Sep 26 2000
Last Updated:	Oct 20 2000

COMMENTS

Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

LIBRARY

Lib Name:	NIH_MGC_71
Organism:	Homo sapiens
Organ:	uterus
Tissue type:	leiomyosarcoma
Lab host:	DH10B (phage-resistant)
Vector:	pCMV-SPORT6
R. Site 1:	NotI

R. Site 2: SalI
Description: Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb.

SUBMITTER

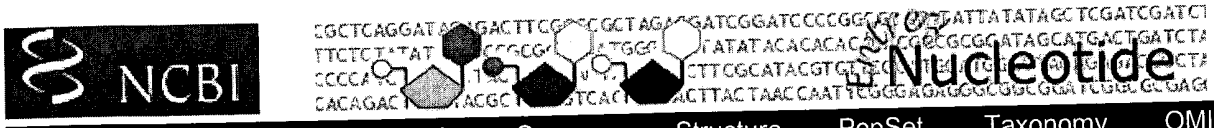
Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Institutes of Health, Mammalian Gene Collection (MGC)
Authors: NIH-MGC http://mgc.nci.nih.gov/
Year: 1999
Status: Unpublished

MAP DATA

Revised: October 24, 2001.



☐ **1:** AI657485. Fws098 Human feta...[gi:4753575] Taxonomy, LinkOut

IDENTIFIERS

dbEST Id:	**2486129**
EST name:	Fws098
GenBank Acc:	AI657485
GenBank gi:	4753575

CLONE INFO

Clone Id:	(5')
DNA type:	cDNA

PRIMERS

Sequencing:	T3 forword
PolyA Tail:	Unknown

SEQUENCE

AATCCAAGCTCCCAATCACCCACCGCCGCAGCCCCCTACGCAGGCCACGCCACTGATGCA
CACCAAACCCAATAGCCAGGGCCCTCCCAACCCCATGGCATTGCCCAGTGAGCATGGACT
TGAGCAGCCATCTCACACCCCTCCCCAGACTCCAACGCCCCCCAGTACTCCGCCCCTAGG
AAAACAGAACCCCAGTCTGCCAGCTCCTCAGACCCTGGCAGGGGGTAACCCTGAAACTGC
ACAGCCACATGCTGGAACCTTACCGAGACCGAGACCAGTACCAAAGCCAAGGAACCGGCC
CAGCGTGCCCCCACCCCCCCAACCTCCTGGTGTCCACTCAGCTGGGGACAGCAGCCTCAC
CAACACAGCACCAACAGCTTCCAAGATAGTAACAGACTCCAATTCCAGGGTTTCAGAACC
GCATCGCAGCATCTTTCCTGAAATGCACTCAGACTCAGCCAGCAAAGACGTGCCTGGCCG
CATCCTGCTGGATATAGACAATGATACCGAGAGCACTGCCCTGTGAAGAAAGCCCTTTCC
CAGCCCTCCACCACTTCCACCCTGGCGAGTGGAGCAGGGGCAGGCGAACCTCTTTCTTTG
CAGACCGAACAGTGAAAAGCTTTCAGTGGAGGACAAAGGAGGGCCTCACTGTGCGGGACC
TGGCCTTCTGCACGGCCCAAGGAGAACCTGGAGGCCACCACTAAAGCTGAATGACCTGTG
TCTTGAAGAAGTTGGCTTTCTTTACATGGGAAGGAAATCATGCCAAAAAAATCCAAAACA
AAGAAGTACCTGGAGTGGAGAGAGTATTCCTGCTGAAACGCGCATAGGAAGCTTTTGTCC
CTGCTGTTAATGCGGGCAGCACCTACAGCAACTTGGAATGAGTAAGAAGCAGTGCGTTAA
CTATCTATTTAATAAAATGCGCTCATTATGCAAGTCGCCTACTCTCTGCTACCTGGACGT
TCATTCTTATGTATTAGGAGGGAGGCTGCGCTCCTTCAGACTTGCTGCAGAATCATTTTG
TATCATGTATGGTCTGTGTCTCCCCAGTCCCCTCAGAACCATGCCCATGGATGGTGACTG
CTGGCTCTGTCACCTCATCAAACTGGATGTGACCCATGCCGCCTCGTTGGATTGTCGGAA
TGTAGACAGAAATGTACTGTTCTTTTTTTTTTTTTTAAACAATGTAATTGCTACTTGATA
AGGACCGAACATTATTCTAGTTTCATGTTTAATTTGAATTAAATATATTCTGTGGTTTAT
ATGAAAACTTCAAAAAAAAAAAAAAAAAACTCGAGAGTACTTCTAGAGCGGCCGCGGGCC
CATCGATTTTCCACCCGGGTGGGGTACCAGGTAAGTGTA

Quality:	High quality sequence stops at base: 1200
Entry Created:	May 5 1999
Last Updated:	May 5 1999

LIBRARY

Lib Name:	Human fetal heart cDNA library
Organism:	Homo sapiens
Tissue type:	heart
Lab host:	E. coli XL1-Blue
Vector:	Lambda ZAP Express
R. Site 1:	EcoRI

R. Site 2: XhoI
Description: mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express.

SUBMITTER

Name: ZhiMing Zhu
Lab: Hypertension Center and Division of Cardiology
Institution: Daping Hospital, Third Military Medical University
Address: Chongqing 400042, People's Republic of China
Tel: 0086-23-68757745
Fax: 0086-23-68705094
E-mail: zhuzm@yaho.com or zhuzm@public.cta.cq.cn

CITATIONS

Title: Differential screening captopril responsive genes in heart from spontaneously hypertensive rats
Authors: Zhu,Z., Liu,Y., Xu,Y., Meng,X., Zhao,B., Zhu,S.
Year: 1999
Status: Unpublished

MAP DATA

Revised: October 24, 2001.

WEST Search History

DATE: Tuesday, July 09, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=JPAB,EPAB,DWPI; PLUR=NO; OP=ADJ			
L32	L31 and (ras adj like)	0	L32
L31	l24 or l23	130	L31
L30	l25 and (ras adj like)	0	L30
L29	l26 and (ras adj like)	0	L29
L28	L27 and (ras adj like)	0	L28
L27	yan$[in]	33935	L27
L26	beasley$[in]	566	L26
L25	ketchum$[in]	108	L25
L24	(di francesco$)[in]	58	L24
L23	(difrancesco$)[in]	72	L23
DB=PGPB; PLUR=NO; OP=ADJ			
L22	(celera genomics corporation)[as]	0	L22
DB=USPT; PLUR=NO; OP=ADJ			
L21	(celera genomics corporation)[as]	0	L21
L20	(celera genomics corporation)[asn]	0	L20
L19	celera$[as]	0	L19
L18	celera$[asn]	0	L18
L17	cellera[asn]	0	L17
L16	L6 and l1	2	L16
L15	L5 and l1	0	L15
L14	L7 and l1	0	L14
L13	L11 and GTPase$1	0	L13
L12	L11 and l1	0	L12
L11	L10 or l9	72	L11
L10	(difrancesco$)[in]	44	L10
L9	(di francesco$)[in]	28	L9
L8	(di francesco$)[au]	0	L8
L7	beasley$[in]	305	L7
L6	yan$[in]	10764	L6
L5	ketchum$[in]	57	L5
L4	L1 with teratocarcinoma$1	8	L4
L3	L2 and @ad<20010129	22	L3

L2	L1 and teratocarcinoma$1	22	L2
L1	ras adj like	87	L1

END OF SEARCH HISTORY

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT 15:19:03 ON 09 JUL 2002

L8	350284	S	YAN?/AU
L9	0	S	L8 AND NADRIN#
L10	26	S	L8 AND (RAS(W)LIKE)
L11	1054	S	KETCHUM?/AU
L12	1550	S	(DI FRANCESCO?)/AU OR DIFRANCESCO?/AU
L13	4464	S	BEASLEY?/AU
L14	6870	S	L11 OR L12 OR L13
L15	0	S	L14 AND (NADRIN# OR (RAS(W)LIKE))
L16	10		DUP REM L10 (16 DUPLICATES REMOVED)
L17	164	S	L8 AND (VIRTUAL)
L18	0	S	L8 AND (VIRTUAL(3A)NORTHERN)
L19	0	S	L14 AND (VIRTUAL(3A)NORTHERN)

L3 ANSWER 1 OF 2 CANCERLIT
ACCESSION NUMBER: 93686556 CANCERLIT
DOCUMENT NUMBER: 93686556
TITLE: Identification and characterization of five novel RAS family genes expressed in a human **teratocarcinoma** cell line.
AUTHOR: Drivas G T
CORPORATE SOURCE: New York Univ.
SOURCE: Diss Abstr Int [B], (1992). Vol. 52, No. 12, pp. 6225. ISSN: 0419-4217.
DOCUMENT TYPE: (THESIS)
FILE SEGMENT: ICDB
LANGUAGE: English
ENTRY MONTH: 199301

AB The RAS gene family codes for a group of low-mol wt (21-25 kD) GTP-binding and hydrolyzing proteins. On the basis of amino acid sequence homology, RAS family genes have been divided into four major groups, termed true RAS, **RAS-like**, RHO and YPT/RAB. Members of the RAS family have been implicated in the regulation of cell growth and division (true RAS), the regulation of vesicle transport (YPT/RAB), and in the maintenance of cell structure (RHO). All RAS family proteins share four highly conserved domains involved in guanine nucleotide binding. We applied two different approaches, both based on the use of oligonucleotides specific for these functional coding domains, to isolate novel human members of each of the major groups of the RAS family. They are TC21 (**RAS-like** subfamily), TC25 and TC10 (RHO subfamily), YL8 (YPT/RAB subfamily) and TC4, a gene whose distinctive characteristics suggest that it defines a new branch of this gene family. Characterization of the isolated cDNAs indicates that these genes are well conserved in mammals, and in some cases, highly homologous to proteins (70-80% identity) recently isolated from fission yeast. Northern analysis of a variety of human and murine cell types reveals markedly different patterns of transcription for these genes; TC4, TC25 and YL8 are generally widely expressed, while TC10 and TC21 are more restricted in their distribution. The cDNAs are capable of encoding proteins in the range of 21-25 kD, and one of these, YL8, has demonstrated GTP-binding ability. Wild-type and mutagenized versions (carrying mutations like those found in RAS oncoproteins) of TC4, TC21, and TC25 do not show transforming potential in transfected NIH 3T3 fibroblasts. This suggests that their regulatory roles differ from those of true RAS proteins. In the case of TC25, stably transfected 3T3 cell lines overexpressing this cDNA product display an altered cellular morphology, a finding consistent with the proposed role of RHO group proteins. (Full text available from University Microfilms International, Ann Arbor, MI, as Order No. AAD92-13224)

L7 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:74241 CAPLUS
DOCUMENT NUMBER: 122:47573
TITLE: Identification of novel **ras** family genes in a human teratocarcinoma cell line by oligonucleotide screening
AUTHOR(S): **Drivas, George T.**; Rush, Mark G.; D'Eustachio, Peter
CORPORATE SOURCE: Sch. Med., New York Univ., New York, NY, USA
SOURCE: ras Superfamily GTPases (**1993**), 329-47. Editor(s): Lacal, Juan Carlos; McCormick, Frank. CRC: Boca Raton, Fla.
CODEN: 60MXA3
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A review with 53 refs.

L7 ANSWER 8 OF 11 MEDLINE DUPLICATE 5

ACCESSION NUMBER: 91248193 MEDLINE
DOCUMENT NUMBER: 91248193 PubMed ID: 2039498
TITLE: Evolutionary grouping of the **RAS**-protein family.
AUTHOR: **Drivas G T**; Palmieri S; D'Eustachio P; Rush M G
CORPORATE SOURCE: Department of Biochemistry, New York University School of Medicine, New York 10016.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, **(1991 May 15)** 176 (3) 1130-5.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199107
ENTRY DATE: Entered STN: 19910719
Last Updated on STN: 20000303
Entered Medline: 19910703

AB Over 50 proteins related to the mammalian H-, K-, and N-**RAS** GTP binding and hydrolyzing proteins are known. These relatively low molecular weight proteins are usually grouped into four subfamilies, termed true **RAS**, **RAS**-like, RHO, and RAB/YPT, based on the presence of shared amino acid sequence motifs in addition to those involved in guanine nucleotide binding. Here, we apply parsimony analysis to the overall amino acid sequences of these proteins to infer possible phylogenetic relationships among them.